

**ATTACHMENT A**  
**(Blast 2 Sequences Results)**



# Blast 2 Sequences results

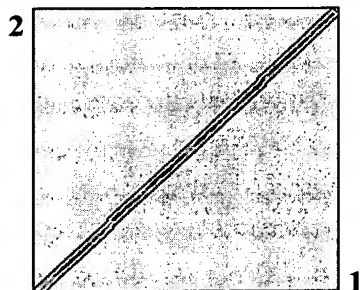
[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.9 [May-01-2004]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**  
x\_dropoff: **50** expect: **10.000** wordsize: **3** Filter ☒ Align

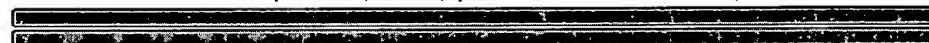
Sequence 1 gi [16324](#) histone H3.3 like protein [Arabidopsis thaliana] Length 136 (1 .. 136)

Sequence 2 gi [30315015](#) histone H3.3 [Vitis vinifera] Length 136 (1 .. 136)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 266 bits (679), Expect = 1e-70  
Identities = 136/136 (100%), Positives = 136/136 (100%)



```
Query:      1  MARTKQTARKSTGGKAPRKQLATKAARKSAPTTGGVKKPHRYRPGTVALREIRKYQKSTE  60
             MARTKQTARKSTGGKAPRKQLATKAARKSAPTTGGVKKPHRYRPGTVALREIRKYQKSTE
Sbjct:      1  MARTKQTARKSTGGKAPRKQLATKAARKSAPTTGGVKKPHRYRPGTVALREIRKYQKSTE  60
Histone H3  34  *****

Query:      61  LLIRKLPFQRLVREIAQDFKTDLRFSHAVLALQEAAEAYLVGLFEDTNLCAIHAKRVTI  120
             LLIRKLPFQRLVREIAQDFKTDLRFSHAVLALQEAAEAYLVGLFEDTNLCAIHAKRVTI
Sbjct:      61  LLIRKLPFQRLVREIAQDFKTDLRFSHAVLALQEAAEAYLVGLFEDTNLCAIHAKRVTI  120
Histone H3  61  *****

Query:      121 MPKDIQLARRIRGERA  136
             MPKDIQLARRIRGERA
Sbjct:      121 MPKDIQLARRIRGERA  136
Histone H3  121 *****
```

CPU time: 0.02 user secs. 0.01 sys. secs 0.03 total secs.

Lambda	K	H
0.321	0.132	0.367

Gapped Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62  
Gap Penalties: Existence: 11, Extension: 1  
Number of Sequences: 1  
Number of Hits to DB: 284  
Number of extensions: 94  
Number of successful extensions: 1  
Number of sequences better than 10.0: 1



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## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.9 [May-01-2004]

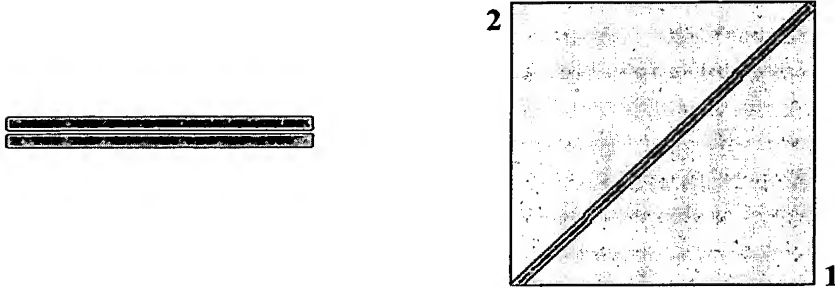
Matrix: **BLOSUM62** gap open: **11** gap extension: **1**  
 x\_dropoff: **50** expect: **10.000** wordsize: **3** Filter ☒ Align:

Sequence 1 gi 16324 histone H3.3 like protein [Arabidopsis thaliana]

Length 136 (1 .. 136)

Sequence 2 gi 42541263 putative histone H3 [Oryza sativa (japonica cultivar-group)]

Length 136 (1 .. 136)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 266 bits (679), Expect = 1e-70  
 Identities = 136/136 (100%), Positives = 136/136 (100%)

```

Query:      1  MARTKQTARKSTGGKAPRKQLATKAARKSAPTTGGVKKPHRYRPGTVALREIRKYQKSTE  60
             MARTKQTARKSTGGKAPRKQLATKAARKSAPTTGGVKKPHRYRPGTVALREIRKYQKSTE
Sbjct:      1  MARTKQTARKSTGGKAPRKQLATKAARKSAPTTGGVKKPHRYRPGTVALREIRKYQKSTE  60
Histone H3  34  *****

Query:      61  LLIRKLPFQRLVREIAQDFKTDLRFSHAVLALQEAAEAYLVGLFEDTNLCAIHAKRVTI  120
             LLIRKLPFQRLVREIAQDFKTDLRFSHAVLALQEAAEAYLVGLFEDTNLCAIHAKRVTI
Sbjct:      61  LLIRKLPFQRLVREIAQDFKTDLRFSHAVLALQEAAEAYLVGLFEDTNLCAIHAKRVTI  120
Histone H3  61  *****

Query:      121 MPKDIQLARRIGERA 136
             MPKDIQLARRIGERA
Sbjct:      121 MPKDIQLARRIGERA 136
Histone H3  121 *****
  
```

CPU time: 0.01 user secs. 0.00 sys. secs 0.01 total secs.

Lambda K H  
 0.321 0.132 0.367

Gapped  
 Lambda K H  
 0.267 0.0410 0.140

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